

Table 1: Unprecedented Flexibility for Multiple Applications

Application	High Output Flow Cell Configuration		Mid Output Flow Cell Configuration	
	No. of Samples	Time	No. of Samples	Time
Gene Expression Profiling > 10 M Reads 1 × 75 bp	40	11 hours	N/A	N/A
mRNA-Seq > 40 M Reads 2 × 75 bp	10	18 hours	3	15 hours
Enrichment Panel 12 Mb Region > 20x coverage at > 95% targets	N/A	N/A	20	26 hours
Whole-Exome Sequencing > 90% at > 10x coverage	9	18 hours	3	15 hours
Human Whole-Genome Sequencing 3 GB Genome > 30x coverage 2 × 150 bp	1	29 hours	N/A	N/A

offers customers access to the broadest ecosystem of established protocols, workflows, data sets, and data analysis tools.

Industry-Leading SBS Chemistry Delivers Highest Accuracy

At the core of the NextSeq 500 System is industry-leading Illumina SBS chemistry—the most widely adopted NGS technology. This proprietary reversible terminator-based method enables the massively parallel sequencing of millions of DNA fragments, detecting single bases as they are incorporated into growing DNA strands. The method virtually eliminates errors and missed calls associated with strings of repeated nucleotides (homopolymers).

Furthermore, the latest evolution in sequencing chemistry—SBS v2 sequencing reagents—enable the NextSeq 500 System to deliver the most accurate human genome, exome, or transcriptome at any coverage level. The NextSeq 500 System with SBS v2 chemistry delivers improved signal intensities and the lowest number of false positives, false negatives, and error rates yet. This exceptional data quality sets Illumina systems apart and gives researchers full confidence in the data generated.

Versatile and Flexible to Support the Widest Range of Applications

The NextSeq 500 System is the right sequencer for any project size and sequencing throughput, providing users with optimal operational efficiency. It is the only desktop sequencing system capable of sequencing a high-coverage (30x) whole human genome in one run. The NextSeq 500 System also delivers a one-day turnaround for a number of popular sequencing applications. With this instrument, researchers can sequence:

- 1–16 exomes/run
- 1–20 transcriptomes/run

- 6–96 targeted panels/run
- 12–40 gene expression profiling samples/run

The NextSeq 500 System is easily configured providing researchers with scalability to handle low to high-throughput project sizes for maximum operational efficiency. Based on sample volume and coverage needs, researchers can choose between two flow cell configurations (High Output and Mid Output), easily shifting from low to higher throughput processing with each sequencing run (Table 1). The NextSeq 500 System provides integrated support for paired-end sequencing, offering user-defined read lengths up to 2 × 150 bp.

The system is supported by the full suite of Illumina library prep and target enrichment solutions, offering library compatibility across the Illumina sequencing portfolio. This allows researchers to scale-up

Figure 3: Illumina NGS Portfolio Makes Sequencing Accessible to All Researchers



Illumina NGS systems offer solutions for every application, sample type, and sequencing scale. Each delivers high data quality and accuracy with flexible throughput and simple, streamlined workflows. Data can be seamlessly compared, exchanged, and analyzed in BaseSpace.

¹Q30 = 1 error in 1,000 base calls or an accuracy of 99.9%

studies easily to the higher throughput HiSeq® System or perform follow-up studies on the MiSeq® System (Figure 3).

NextSeq 550 Enables Array Scanning

The NextSeq 550 System combines microarray scanning with the proven and robust NextSeq 500 sequencing system.*† By leveraging microarray scanning on the NextSeq 550 System, researchers have instant access to a powerful, complementary technology for further exploration or confirmation of copy number variants detected through sequencing. With the NextSeq 550 System, the menu of cutting-edge research applications is maximized while the instrument costs are simultaneously minimized. The NextSeq 550 System supports flexible options by enabling a broad range of applications in reproductive, genetic health, and oncology-related research.

Streamlined Bioinformatics

The NextSeq 500 System supports a number of data analysis options. Primary data analyses, including base calling and quality scoring, are performed by integrated instrument computers. Sequencing run data can be run through a wide range of open-source or commercial pipelines developed for Illumina data, or instantly transferred, analyzed, and stored securely in BaseSpace® (Cloud or Onsite), the Illumina genomics computing environment. BaseSpace downstream data analysis includes alignment and variant detection, annotation, visualization, and interpretation.

BaseSpace also includes Illumina-developed data analysis apps for exome, transcriptome, whole-genome, and somatic variant calling. Thanks to Illumina's industry-standard data formats, third-party developers have created a rich ecosystem of commercial and open-source tools for more extensive downstream data analysis.

Summary

The NextSeq 500 and NextSeq 550 Systems are transformative sequencers that enable NGS to become an everyday tool in laboratories worldwide. Incorporating the latest advancements in SBS chemistry, the flexible NextSeq Systems push-button operation and

* Microarray scanning is only supported on the NextSeq 550 System.
 † Microarray scanning enabled Q2 2015 and will include support for the CytoSNP-850k, CytoSNP-12, and Karyomap-12 DNA microarrays.

Join the Illumina Community

With a NextSeq 500 or 550 System in their laboratory, researchers join a worldwide community of over 60,000 scientists using Illumina technology for their research studies. Illumina schedules community events throughout the year, bringing researchers together to share ideas. User group meetings, scientific symposiums, and blog forums provide venues to discuss new research methods and breakthrough studies.

An integral part of the Illumina community is our dedicated service and support team, consisting of more than 300 people worldwide, 75% of whom have advanced degrees. Illumina technical support begins when the NextSeq 500 System is delivered, with Illumina scientists and engineers assisting with system installation and setup, and the training of laboratory personnel. They are there 24/7 globally to answer questions every step of the way, giving researchers the peace of mind to focus on their next research study.

As researchers' needs change, new systems are brought into the laboratory, or new methods are undertaken, the Illumina support and training teams are there to provide assistance. In addition to on-site support, training courses (via webinar or at an Illumina facility) are available to bring laboratory personnel quickly up to speed.

streamlined sample-to-results workflow allow researchers to perform the most popular high-throughput applications in less than a day. Its multiple flow cell and reagent configurations enable low-throughput sequencing as needed, providing researchers with the operating efficiency to handle a range of project sizes.

Learn More

Go to www.illumina.com/systems/nextseq-sequencer.ilmn to learn more about the next revolution in sequencing.

NextSeq Series Performance Parameters[§]

Flow Cell Configuration	Read Length (bp)	Output (Gb)	Run Time	Data Quality	Required Input
High Output Flow Cell	2 × 150	100–120	29 hours	> 75% > Q30	100 ng–1 µg with TruSeq® Library Prep Kits
Up to 400 M single reads	2 × 75	50–60	18 hours	> 80% > Q30	
Up to 800 M paired-end reads	1 × 75	25–30	11 hours	> 80% > Q30	
Mid Output Flow Cell	2 × 150	32–39	26 hours	> 75% > Q30	
Up to 130 M single reads	2 × 75	16–19	15 hours	> 80% > Q30	
Up to 260 M paired-end reads					

[§]Total times include cluster generation, sequencing, and base calling on a NextSeq 500 System. Install specifications are based on Illumina PhiX control library at supported cluster densities (between 129 and 165 k/mm² clusters passing filter). Actual performance parameters may vary based on sample type, sample quality, and clusters passing filter. The percentage of bases > Q30 is averaged over the entire run.



